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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/676,380A

DATE: 04/20/2001

TIME: 07:49:17

Input Set : A:\ES.txt

Output Set: N:\CRF3\04202001\I676380A.raw

ENTERED

2 <110> APPLICANT: Maihle, Nita Reiter, Jill Baron, Andre  
 W--> 3 <120> TITLE OF INVENTION: SOLUBLE EPIDERMAL GROWTH FACTOR RECEPTOR-LIKE PROTEINS AND THEIR USES  
 IN  
 W--> 4 CANCER DETECTION METHODS  
 W--> 5 <130> FILE REFERENCE: TBIG  
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/676,380A  
 C--> 6 <141> CURRENT FILING DATE: 2000-09-29  
 W--> 6 <160> NUMBER OF SEQ ID: 20  
 7 <170> SOFTWARE: PatentIn version 3.0  
 W--> 8 <210> SEQ ID NO: 1  
 9 <211> LENGTH: 705  
 10 <212> TYPE: PRT  
 11 <213> ORGANISM: homo sapiens  
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 15 1 5 10 15  
 17 Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln  
 18 20 25 30  
 20 Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe  
 21 35 40 45  
 23 Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn  
 24 50 55 60  
 26 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys  
 27 65 70 75 80  
 29 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val  
 30 85 90 95  
 32 Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr  
 33 100 105 110  
 35 Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn  
 36 115 120 125  
 38 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu  
 39 130 135 140  
 41 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu  
 42 145 150 155 160  
 44 Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met  
 45 165 170 175  
 47 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro  
 48 180 185 190  
 50 Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln  
 51 195 200 205  
 53 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg  
 54 210 215 220  
 56 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys  
 57 225 230 235 240  
 59 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp  
 60 245 250 255  
 62 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro  
 63 260 265 270

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65 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly  
 66 275 280 285  
 68 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His  
 69 290 295 300  
 71 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu  
 72 305 310 315 320  
 74 Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val  
 75 325 330 335  
 77 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn  
 78 340 345 350  
 80 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp  
 81 355 360 365  
 83 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr  
 84 370 375 380  
 86 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu  
 87 385 390 395 400  
 89 Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp  
 90 405 410 415  
 92 Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln  
 93 420 425 430  
 95 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu  
 96 435 440 445  
 98 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser  
 99 450 455 460  
 101 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu  
 102 465 470 475 480  
 104 Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu  
 105 485 490 495  
 107 Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro  
 108 500 505 510  
 110 Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn  
 111 515 520 525  
 113 Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Lys Leu Leu Glu Gly  
 114 530 535 540  
 116 Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro  
 117 545 550 555 560  
 119 Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro  
 120 565 570 575  
 122 Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val  
 123 580 585 590  
 125 Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp  
 126 595 600 605  
 128 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys  
 129 610 615 620  
 131 Thr Tyr Gly Pro Gly Asn Glu Ser Leu Lys Ala Met Leu Phe Cys Leu  
 132 625 630 635 640  
 134 Phe Lys Leu Ser Ser Cys Asn Gln Ser Asn Asp Gly Ser Val Ser His  
 135 645 650 655  
 137 Gln Ser Gly Ser Pro Ala Ala Gln Glu Ser Cys Leu Gly Trp Ile Pro

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138	660	665	670			
140	Ser Leu Leu Pro Ser Glu Phe Gln Leu Gly Trp Gly Gly Cys Ser His					
141	675	680	685			
143	Leu His Ala Trp Pro Ser Ala Ser Val Ile Ile Thr Ala Ser Ser Cys					
144	690	695	700			
146	His					
147	705					
149	<210> SEQ ID NO: 2					
150	<211> LENGTH: 2850					
151	<212> TYPE: DNA					
152	<213> ORGANISM: homo sapiens					
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154	ccggcgca	cgagcctccg	ccccccgcac	ggtgtgagcg	ccgcgcgcgg	60
156	ccgaggcggc	cggagtcccg	agctagcccc	gcgcggccgc	gccgcggaga	120
158	ggccaccccg	tgcggctccg	cccggatccc	ccgcctcgccg	ccaacccac	180
160	cacggccccc	tgactccgtc	cagtattgtat	ccggagagcc	ggagcgagct	240
162	cagcgatgcg	accctccggg	acggccgggg	cagcgctcc	ggcgctgtc	300
164	gccccggcag	tcgggctctg	gaggaaaaga	aagtggccaa	aggcacaggt	360
166	cgcgttggg	cacttttggaa	gatcattttc	tgcggctcc	gaggatgttc	420
168	agggtggct	tgggaatttgc	gaaattacct	atgtgcagag	gaattatgtat	480
170	taaagaccat	ccaggagggt	gctgttatg	tcctcattgc	cctcaacaca	540
172	ttcctttggaa	aaacctgcag	atcatcagag	gaaatatgtat	gtggagcgaa	600
174	tagcgtt	atctaactat	gatgaaataa	aaaccggact	gaaggagctg	660
176	atttacagga	aatcctgcat	ggcggcgtgc	ggttcagcaa	ccatgcac	720
178	tggagagcat	ccagtggcg	gacatagtca	gcagtgtactt	tctcagcaac	780
180	acttccagaa	ccacccgggc	agctgaaaa	aatgtgtatcc	aatgggagct	840
182	gctgggggtgc	aggagaggag	aactgccaga	aactgaccaa	aatcatctgt	900
184	gctccggcgc	ctggcggtgc	aagtccccc	gtgactgtcg	ccacaaccag	960
186	gctcacaagg	ccccccggag	agcgtactgcc	ttgtctgccc	ttgtgtcaac	1020
188	cgtcaagga	cacccgtcccc	ccactcatgc	tctacaaccc	caccacgtac	1080
190	tgaaccccgaa	ggcaaaatac	agctttgggt	ccacccgtcg	gaagaatgt	1140
192	atgtgggtac	agatcacggc	tgcgtgtcc	gaggcctgtgg	ggccgcacgc	1200
194	aggaaagacgg	cgtccgcaag	tgtaaagaatg	gcgaaaggcc	ttggccaaa	1260
196	gaataggtat	tggtaattt	aaagactcac	tctccataaa	tgctacaaat	1320
198	tcaaaaaactg	cacccatc	agtggcgatc	tccacatcc	ggccgggtggca	1380
200	actccctcac	acataactcct	cctctggatc	cacaggaact	ggatattctg	1440
202	aggaaatcac	agggttttttgc	ctgattcagg	tttggcctga	aaacaggacg	1500
204	cctttggaa	ccttagaaatc	atacgccgc	ggaccaagca	acatggtcag	1560
206	cagtcgtcag	cctgaacata	acatccctgg	gattacgtctc	cctcaaggag	1620
208	gagatgtat	aatttcagga	aacaaaaatt	tgtgtatgc	aaataacaata	1680
210	aactgtttgg	gaccccggt	cagaaaaacca	aaattataag	caacagaggt	1740
212	gcaaggccac	aggccaggc	tgccatgcct	tgtgtcccc	cgaggcgtgc	1800
214	agcccaggaa	ctgcgtctt	tgccggatg	tgcggcagg	caggaaatgc	1860
216	gcaagttct	ggagggtgag	ccaagggagt	ttgtggagaa	ctctgtgtc	1920
218	accaggatgc	cctgcctc	gccatgaaca	tcacccgtac	aggacgggg	1980
220	gtatccagtg	tgcggactac	attgacggcc	ccactgtcg	ccggcaggag	2040
222	tcatgggaga	aaacaacacc	ctggcttggaa	agtagcgcaga	ccggccat	2100
224	tgtgtccatcc	aaactgcacc	tacggccag	gaaatgagag	gtgtgtccacc	2160
226	gcctttttaa	actatcatcc	tgtatcaaa	gtatgtatgg	caccagagcg	2220

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228	ggagccgc	tgctcaggag	tcatgcttag	gatggatccc	ttctctctg	ccgtcagagt	2280
230	ttcagctgg	ttggggtgg	tgccagccacc	tccatgcctg	gccttcgtca	tctgtatca	2340
232	tcacggc	c	ctcctgccac	tgaggctcat	gccttcacgt	gtctgtccc	2400
234	cttctgcca	ccccgtc	ac	tgggccgca	ggttccaaga	gtatccattacc	2460
236	cttccactcc	cttgc	ca	ggttccat	gctaaccatc	accccccagg	2520
238	ctgac	cttgc	cc	ggttccat	acagaatttg	tcaaaaac	2580
240	gcaggga	catgctgcca	gccttc	taatttagcat	ggccccagtc	catgttcta	2640
242	gccttggtt	c	ttctgcccc	tctgttgaa	attctagagc	cagctgtggg	2700
244	gtgtcaa	aaag	ccagatgtga	aaacatctca	ataacaaact	ggctgctttg	2760
246	gaacaacg	cc	tgtcacagag	tagaaactca	aaaatatttg	ctgagtgaat	2820
248	ataaaat	gcat	aataaataat	taaccaccaa			2850

251 <210> SEQ ID NO: 3

252 <211> LENGTH: 641

253 <212> TYPE: PRT

254 <213> ORGANISM: homo sapiens

W--> 255 <400> SEQUENCE: 3

257	Met	Arg	Pro	Ser	Gly	Thr	Ala	Gly	Ala	Ala	Leu	Leu	Ala	Leu	Leu	Ala
258	1				5				10				15			
260	Ala	Leu	Cys	Pro	Ala	Ser	Arg	Ala	Leu	Glu	Glu	Lys	Lys	Val	Cys	Gln
261							20			25			30			
263	Gly	Thr	Ser	Asn	Lys	Leu	Thr	Gln	Leu	Gly	Thr	Phe	Glu	Asp	His	Phe
264							35			40			45			
266	Leu	Ser	Leu	Gln	Arg	Met	Phe	Asn	Asn	Cys	Glu	Val	Val	Leu	Gly	Asn
267							50			55			60			
269	Leu	Glu	Ile	Thr	Tyr	Val	Gln	Arg	Asn	Tyr	Asp	Leu	Ser	Phe	Leu	Lys
270	65						70			75			80			
272	Thr	Ile	Gln	Glu	Val	Ala	Gly	Tyr	Val	Leu	Ile	Ala	Leu	Asn	Thr	Val
273							85			90			95			
275	Glu	Arg	Ile	Pro	Leu	Glu	Asn	Leu	Gln	Ile	Ile	Arg	Gly	Asn	Met	Tyr
276							100			105			110			
278	Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala	Val	Leu	Ser	Asn	Tyr	Asp	Ala	Asn
279							115			120			125			
281	Lys	Thr	Gly	Leu	Lys	Glu	Leu	Pro	Met	Arg	Asn	Leu	Gln	Glu	Ile	Leu
282							130			135			140			
284	His	Gly	Ala	Val	Arg	Phe	Ser	Asn	Asn	Pro	Ala	Leu	Cys	Asn	Val	Glu
285	145						145			150			155			160
287	Ser	Ile	Gln	Trp	Arg	Asp	Ile	Val	Ser	Ser	Asp	Phe	Leu	Ser	Asn	Met
288							165			170			175			
290	Ser	Met	Asp	Phe	Gln	Asn	His	Leu	Gly	Ser	Cys	Gln	Lys	Cys	Asp	Pro
291							180			185			190			
293	Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln
294							195			200			205			
296	Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg
297							210			215			220			
299	Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys
300	225						225			230			235			240
302	Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp
303							245			250			255			
305	Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro

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306	260	265	270	
308	Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly			
309	275	280	285	
311	Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His			
312	290	295	300	
314	Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu			
315	305	310	315	320
317	Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val			
318	325	330	335	
320	Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn			
321	340	345	350	
323	Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp			
324	355	360	365	
326	Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr			
327	370	375	380	
329	Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu			
330	385	390	395	400
332	Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp			
333	405	410	415	
335	Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln			
336	420	425	430	
338	His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu			
339	435	440	445	
341	Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser			
342	450	455	460	
344	Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu			
345	465	470	475	480
347	Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu			
348	485	490	495	
350	Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro			
351	500	505	510	
353	Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn			
354	515	520	525	
356	Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Lys Leu Leu Glu Gly			
357	530	535	540	
359	Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro			
360	545	550	555	560
362	Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro			
363	565	570	575	
365	Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val			
366	580	585	590	
368	Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp			
369	595	600	605	
371	Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys			
372	610	615	620	
374	Thr Tyr Gly Pro Gly Asn Glu Ser Leu Lys Ala Met Leu Phe Cys Leu			
375	625	630	635	640
377	Phe			
380	<210> SEQ ID NO: 4			

## VERIFICATION SUMMARY

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Input Set : A:\ES.txt

Output Set: N:\CRF3\04202001\I676380A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:270 C: Current Application Number differs, Replaced Current Application No  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:6 M:283 W: Missing Blank Line separator, <160> field identifier  
L:8 M:283 W: Missing Blank Line separator, <210> field identifier  
L:12 M:283 W: Missing Blank Line separator, <400> field identifier  
L:153 M:283 W: Missing Blank Line separator, <400> field identifier  
L:255 M:283 W: Missing Blank Line separator, <400> field identifier  
L:384 M:283 W: Missing Blank Line separator, <400> field identifier  
L:525 M:283 W: Missing Blank Line separator, <400> field identifier  
L:666 M:283 W: Missing Blank Line separator, <400> field identifier  
L:807 M:283 W: Missing Blank Line separator, <400> field identifier  
L:815 M:283 W: Missing Blank Line separator, <400> field identifier  
L:823 M:283 W: Missing Blank Line separator, <400> field identifier  
L:831 M:283 W: Missing Blank Line separator, <400> field identifier  
L:839 M:283 W: Missing Blank Line separator, <400> field identifier  
L:847 M:283 W: Missing Blank Line separator, <400> field identifier  
L:855 M:283 W: Missing Blank Line separator, <400> field identifier  
L:863 M:283 W: Missing Blank Line separator, <400> field identifier  
L:875 M:283 W: Missing Blank Line separator, <400> field identifier  
L:887 M:283 W: Missing Blank Line separator, <400> field identifier  
L:899 M:283 W: Missing Blank Line separator, <400> field identifier  
L:908 M:283 W: Missing Blank Line separator, <400> field identifier  
L:920 M:283 W: Missing Blank Line separator, <400> field identifier  
L:932 M:283 W: Missing Blank Line separator, <400> field identifier